GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 27, 2001, 18:11:29 ; Search time 4492.43 Seconds
(without alignments)
6503.779 Million cell updates/sec

Title: US-09-830-647-4
Perfect score: 2719
Sequence: 1 aattcggcacgagctctctg.....aaaaaaaaaaaaaactcgag 2719

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 11351937 seqs, 5372889281 residues

Total number of hits satisfying chosen parameters: 22703874

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: em_estfun:*
2: em_esthum:*
3: em_estin:*
4: em_estom:*
5: em_estpl:*
6: em_estba:*
7: em_estro:*
8: em_estov:*
9: em_htc:*
10: gb_est1:*
11: gb_est2:*
12: gb_htc:*
13: gb_gss:*
14: em_gss_fun:*
15: em_gss_hum:*
16: em_gss_inv:*
17: em_gss_pln:*
18: em_gss_pro:*
19: em_gss_rod:*
20: em_gss_vrt:*
21: em_gss_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	887.6	32.6	950	10	AL560180	AL560180 AL560180
c	2	817	30.0	845	10	AL581669	AL581669 AL581669
	3	769	28.3	769	10	AL548911	AL548911 AL548911
c	4	768.2	28.3	784	10	AL573294	AL573294 AL573294
	5	753.4	27.7	1019	11	BG720949	BG720949 602692613
	6	723.4	26.6	725	10	AL559244	AL559244 AL559244
	7	721.6	26.5	903	10	AU128881	AU128881 AU128881
c	8	719	26.4	742	10	AL580899	AL580899 AL580899
c	9	710	26.1	744	10	AI948485	AI948485 wq06d08.x
	10	696.4	25.6	821	11	BG496289	BG496289 602538259
	11	692.4	25.5	703	11	BG716928	BG716928 602689445
	12	691.6	25.4	767	11	BG717397	BG717397 602689740
	13	686	25.2	712	11	BF793466	BF793466 602254949
	14	671.4	24.7	701	10	AW960753	AW960753 EST372824
c	15	661.4	24.3	743	10	AI761101	AI761101 wi69g03.x
c	16	647	23.8	730	10	AW105287	AW105287 xd59f02.x
	17	645.4	23.7	659	10	BE613476	BE613476 601504243
	18	639.4	23.5	927	11	BG025871	BG025871 602292007
	19	607	22.3	2338	12	AK014480	AK014480 Mus muscu
c	20	597.8	22.0	603	10	AI824033	AI824033 wj29g09.x
	21	593	21.8	616	11	BE884320	BE884320 601505790
	22	586	21.6	701	11	BG722508	BG722508 602693762
	23	585	21.5	585	11	BG724408	BG724408 602689338
	24	574.8	21.1	581	11	BG719249	BG719249 602690314
	25	572	21.0	670	10	AV645569	AV645569 AV645569
	26	568.2	20.9	706	11	BI094492	BI094492 602850523
	27	562.8	20.7	950	11	BE888697	BE888697 601513095
	28	561.6	20.7	839	10	BE564084	BE564084 601348046
	29	561	20.6	561	10	AA451820	AA451820 zx46f01.r
	30	560.4	20.6	578	11	BG724066	BG724066 602697046
	31	553	20.3	639	10	AV728361	AV728361 AV728361
	32	548.6	20.2	935	11	BG341292	BG341292 602463961
c	33	548	20.2	549	10	AI923577	AI923577 wn75c03.x
c	34	545.2	20.1	571	10	AU150504	AU150504 AU150504
	35	540.2	19.9	760	11	BF219022	BF219022 601882245
	36	530.4	19.5	629	11	BE888268	BE888268 601511791
	37	523.8	19.3	839	10	BE782351	BE782351 601469844
c	38	493.4	18.1	570	10	AU143969	AU143969 AU143969
c	39	490.4	18.0	493	10	AI452459	AI452459 tj62b12.x
	40	488.6	18.0	626	10	BE245831	BE245831 TCBAP1E31
	41	484.2	17.8	489	10	AW967974	AW967974 EST380049
c	42	478.2	17.6	557	10	AW591976	AW591976 hf36e07.x
c	43	474	17.4	474	10	AI452802	AI452802 tj50f11.x
c	44	470	17.3	470	10	AI217171	AI217171 qf47g10.x
c	45	468.2	17.2	484	10	AI797599	AI797599 we89f04.x

ALIGNMENTS

RESULT 1
AL560180
LOCUS AL560180 950 bp mRNA EST 16-FEB-2001
DEFINITION AL560180 LTI_FL011_BC1 Homo sapiens cDNA clone CS0DG002YE20 5 prime , mRNA sequence.
ACCESSION AL560180
VERSION AL560180.1 GI:12906394
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 950)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES Location/Qualifiers
source 1. .950
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DG002YE20"
/clone_lib="LTI_FL011_BC1"
/sex="male"
/tissue_type="B cells from Burkitt lymphoma"
/lab_host="DH10B"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen

9800 Medical Center Drive Rockville, Maryland 20850, USA
Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com"

BASE COUNT 303 a 204 c 209 g 232 t 2 others
ORIGIN

Query Match 32.6%; Score 887.6; DB 10; Length 950;
Best Local Similarity 99.9%; Pred. No. 4.5e-134;
Matches 887; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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Qy    311 ctttgcgccttcctcctccgcgccttggagccggatccggccccggaaacccgacctgca 370
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Db      1 CTTTGCGCCTTCCTCCTCCGCGCCTTGGAGCCGGATCCGGCCCCGGAAACCCGACCTGCA 60

Qy    371 gacgcggtacctctactgcgtagaggccgtagctggcggaaggagagaggcggccgtcct 430
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Db     61 GACGCGGTACCTCTACTGCGTAGAGGCCGTAGCTGGCGGAAGGAGAGAGGCGGCCGTCCT 120

Qy    431 gtcaacaggccgggggaagccgtgctttcgcggctgcccggtgcgacactttctccggac 490
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Db    121 GTCAACAGGCCGGGGGAAGCCGTGCTTTCGCGGCTGCCCGGTGCGACACTTTCTCCGGAC 180

Qy    491 ccagcatgtaggtgccgggcgactgccatgaactccggagccatgaggatccacagtaaa 550
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CCAGCATGTAGGTGCCGGGCGACTGCCATGAACTCCGGAGCCATGAGGATCCACAGTAAA 240

Qy    551 ggacatttccagggtggaatccaagtcaaaaatgaaaaaaacagaccatctctgaaatct 610
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GGACATTTCCAGGGTGGAATCCAAGTCAAAAATGAAAAAAACAGACCATCTCTGAAATCT 300

Qy    611 ctgaaaactgataacaggccagaaaaatccaaatgtaagccactttggggaaaagtattt 670
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Db    301 CTGAAAACTGATAACAGGCCAGAAAAATCCAAATGTAAGCCACTTTGGGGAAAAGTATTT 360

Qy    671 taccttgacttaccttctgtcaccatatctgaaaaacttcaaaaggacattaaggatctg 730
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Db    361 TACCTTGACTTACCTTCTGTCACCATATCTGAAAAACTTCAAAAGGACATTAAGGATCTG 420

Qy    731 ggagggcgagttgaagaatttctcagcaaagatatcagttatcttatttcaaataagaag 790
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GGAGGGCGAGTTGAAGAATTTCTCAGCAAAGATATCAGTTATCTTATTTCAAATAAGAAG 480

Qy    791 gaagctaaatttgcacaaaccttgggtcgaatttctcctgtaccaagtccagaatctgca 850
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 GAAGCTAAATTTGCACAAACCTTGGGTCGAATTTCTCCTGTACCAAGTCCAGAATCTGCA 540

Qy    851 tatactgcagaaaccacttcacctcatcccagccatgatggaagttcatttaagtcaccca 910
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    541 TATACTGCAGAAACCACTTCACCTCATCCCAGCCATGATGGAAGTTCATTTAAGTCACCA 600

Qy    911 gacacagtgtgtttaagcagaggaaaattattagttgaaaaagctatcaaggaccatgat 970
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Db    601 GACACAGTGTGTTTAAGCAGAGGAAAATTATTAGTTGAAAAAGCTATCAAGGACCATGAT 660

Qy    971 tttattccttcaaatagtatattatcaaatgccttgtcatggggagtaaaaattcttcat 1030
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Db    661 TTTATTCCTTCAAATAGTATATTATCAAATGCCTTGTCATGGGGAGTAAAAATTCTTCAT 720

Qy   1031 attgatgacattagatactacattgaacaaaagaaaaaagagttgtatttactcaagaaa 1090
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Db    721 ATTGATGACATTAGATACTACATTGAACAAAAGAAAAAAGAGTTGTATTTACTCAAGAAA 780

Qy   1091 tcaagtacttcagtaagagatgggggcaaaagagttggtagtggtgcacaaaaaacaaga 1150
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    781 TCAAGTACTTCAGTAAGAGATGGGGGCAAAAGAGTTGGTAGTGGTGCACAAAAAACAAGA 840

Qy   1151 acaggaagactcaaaaagccttttgtaaaggtggaagatatgagccaa 1198
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Db    841 ACAGGAAGACTCAAAAAGCCTTTTGTAAAGGTGGRAGATATGAGCCAA 888
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RESULT 2

AL581669/c
LOCUS AL581669 845 bp mRNA EST 16-FEB-2001
DEFINITION AL581669 LTI_FL011_BC1 Homo sapiens cDNA clone CS0DG002YE20 3 prime , mRNA sequence.
ACCESSION AL581669
VERSION AL581669.1 GI:12948899
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 845)
AUTHORS Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES Location/Qualifiers
source 1. .845
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="CS0DG002YE20"
/clone_lib="LTI_FL011_BC1"
/sex="male"
/tissue_type="B cells from Burkitt lymphoma"
/lab_host="DH10B"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-stranded cDNA was digested with Not I and cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT 216 a 146 c 154 g 307 t 22 others
ORIGIN

Query Match 30.0%; Score 817; DB 10; Length 845;
Best Local Similarity 96.8%; Pred. No. 1.2e-122;
Matches 818; Conservative 22; Mismatches 4; Indels 1; Gaps 1;

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Qy   1622 atacaacagtgaaggagcagaatttcctgtataaagagacccaggaaactgaaaaaaagc 1681
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Db    845 AWACAACAGTGAAGGAGCAGAATTTCCTGTATAAAGAGACCCAGGAAACTGAAAAAAAGC 786

Qy   1682 tcctgtttatttcagagcccatcccccaccccttcaaatgaattgagagggcttaatgaga 1741
          ||||:|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    785 TCCTKTTTATTTCAGAGCCCATCCCCCACCCTTCAAATGAATTGAGAGGGCTTAATGAGA 726

Qy   1742 aaatgagtaataaatgttccatgttaagtacagctgaagatgacataagacagaatttta 1801
          ||||||||||||||||:|||||||||||||||||||||||||||||||||||||||||||
Db    725 AAATGAGTAATAAATGTYCCATGTTAAGTACAGCTGAAGATGACATAAGACAGAATTTTA 666

Qy   1802 cacagctacctctacataaaaacaaacaggaatgcattcttgacatttccgaacacacat 1861
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    665 CACAGCTACCTCTACATAAAAACAAACAGGAATGCATTCTTGACATTTCCGAACACACAT 606

Qy   1862 taagtgaaaatgacttagaagaactaagggtagatcactataaatgtaacatacaggcat 1921
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Db    605 TAAGTGAAAATGACTTAGAAGAACTAAGGGTAGATCACTATAAATGTAACATACAGGCAT 546

Qy   1922 ctgtacatgtttctg-atttcagtacagataatagtggatctcaaccaaaaacagaagtca 1980
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Db    545 CTGTACATGTTTCTGCATTTCAGTACAGATAATAGTGGATCTCAACCAAAACAGAAGTCA 486

Qy   1981 gatactgtgctttttccagcaaaggatctcaaggaaaaggaccttcattcaatatttact 2040
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Qy   2041 catgattctggtctgataacaataaacagttcacaagagcacctaactgttcaggcaaag 2100
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Db    425 CATGATTCTGGTCTGATAACAATAAACAGTTCACAAGAGCACCTAACTGTTCAGGCAAAG 366

Qy   2101 gctccattccatactcctcctgaggaacccaatgaatgtgacttcaagaatatggatagt 2160
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Db    365 GCCCCATTCCMTMCCCCCCCTSMSSMMCCCAATGAATGTSACTTCAAGAATATGGATAGT 306

Qy   2161 ttaccttctggtaaaatacatcgaaaagtgaaaataatattaggacgaaatagaaaagaa 2220
          ||:||:||||||:|||||||||||||||:|:::|||||||||||||||||||||||||||
Db    305 TTMCCBTCTGGTRAAATACATCGAAAAGKGRRRATAATATTAGGACGAAATAGAAAAGAA 246

Qy   2221 aatctggaaccaaatgctgaatttgataaaagaactgaatttattacacaagaagaaaac 2280
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Db    245 AATCTGGAACCAAATGCTGAATTTGATAAAAGAACTGAATTTATTACACAAGAAGAAAAC 186

Qy   2281 agaatttgtagttcaccggtacagtctttactagacttgtttcagactagtgaagagaaa 2340
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Qy   2341 tcagaatttttgggtttcacaagctacacagaaaagagtggtatatgcaatgttttagat 2400
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Db    125 TCAGAATTTTTGGGTTTMACAAGCTACACAGAAAAGAGTGGTATATGCAATGTTTTAGAT 66

Qy   2401 atttgggaagaggaaaattcagataatctgttaacagcgtttttctcgtccccttcaact 2460
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Qy   2461 tctac 2465
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Db      5 TCTAC 1
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LOCUS       AL548911      769 bp    mRNA            EST       16-FEB-2001
DEFINITION  AL548911 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI043YO10 5
            prime, mRNA sequence.
ACCESSION   AL548911
VERSION     AL548911.1  GI:12884384
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 769)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .769
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                     /db_xref="taxon:9606"
                     /clone="CS0DI043YO10"
                     /clone_lib="LTI_NFL006_PL2"
                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      249 a    168 c    170 g    182 t
ORIGIN
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  Query Match           28.3%;  Score 769;  DB 10;  Length 769;
  Best Local Similarity  100.0%;  Pred. No. 6.9e-115;
  Matches  769;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy    339 agccggatccggccccggaaacccgacctgcagacgcggtacctctactgcgtagaggcc 398
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Db      1 AGCCGGATCCGGCCCCGGAAACCCGACCTGCAGACGCGGTACCTCTACTGCGTAGAGGCC 60

Qy    399 gtagctggcggaaggagagaggcggccgtcctgtcaacaggccgggggaagccgtgcttt 458
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Db     61 GTAGCTGGCGGAAGGAGAGAGGCGGCCGTCCTGTCAACAGGCCGGGGGAAGCCGTGCTTT 120

Qy    459 cgcggctgcccggtgcgacactttctccggacccagcatgtaggtgccgggcgactgcca 518
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CGCGGCTGCCCGGTGCGACACTTTCTCCGGACCCAGCATGTAGGTGCCGGGCGACTGCCA 180

Qy    519 tgaactccggagccatgaggatccacagtaaaggacatttccagggtggaatccaagtca 578
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Db    181 TGAACTCCGGAGCCATGAGGATCCACAGTAAAGGACATTTCCAGGGTGGAATCCAAGTCA 240

Qy    579 aaaatgaaaaaaaacagaccatctctgaaatctctgaaaactgataacaggccagaaaaat 638
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 AAAATGAAAAAAACAGACCATCTCTGAAATCTCTGAAAACTGATAACAGGCCAGAAAAAT 300

Qy    639 ccaaatgtaagccactttggggaaaagtattttaccttgacttaccttctgtcaccatat 698
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Db    301 CCAAATGTAAGCCACTTTGGGGAAAAGTATTTTACCTTGACTTACCTTCTGTCACCATAT 360

Qy    699 ctgaaaaacttcaaaaggacattaaggatctgggagggcgagttgaagaatttctcagca 758
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Db    361 CTGAAAAACTTCAAAAGGACATTAAGGATCTGGGAGGGCGAGTTGAAGAATTTCTCAGCA 420

Qy    759 aagatatcagttatcttatttcaaataagaaggaagctaaatttgcacaaaccttgggtc 818
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Db    421 AAGATATCAGTTATCTTATTTCAAATAAGAAGGAAGCTAAATTTGCACAAACCTTGGGTC 480

Qy    819 gaatttctcctgtaccaagtccagaatctgcatatactgcagaaaccacttcacctcatc 878
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Db    481 GAATTTCTCCTGTACCAAGTCCAGAATCTGCATATACTGCAGAAACCACTTCACCTCATC 540

Qy    879 ccagccatgatggaagttcatttaagtcaccagacacagtgtgtttaagcagaggaaaat 938
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Db    541 CCAGCCATGATGGAAGTTCATTTAAGTCACCAGACACAGTGTGTTTAAGCAGAGGAAAAT 600

Qy    939 tattagttgaaaaagctatcaaggaccatgattttattccttcaaatagtatattatcaa 998
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Db    601 TATTAGTTGAAAAAGCTATCAAGGACCATGATTTTATTCCTTCAAATAGTATATTATCAA 660

Qy    999 atgccttgtcatggggagtaaaaattcttcatattgatgacattagatactacattgaac 1058
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    661 ATGCCTTGTCATGGGGAGTAAAAATTCTTCATATTGATGACATTAGATACTACATTGAAC 720

Qy   1059 aaaagaaaaaagagttgtatttactcaagaaatcaagtacttcagtaag 1107
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Db    721 AAAAGAAAAAAGAGTTGTATTTACTCAAGAAATCAAGTACTTCAGTAAG 769
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RESULT   4
AL573294/c
LOCUS       AL573294      784 bp    mRNA            EST       16-FEB-2001
DEFINITION  AL573294 LTI_NFL006_PL2 Homo sapiens cDNA clone CS0DI043YO10 3
            prime, mRNA sequence.
ACCESSION   AL573294
VERSION     AL573294.1  GI:12932397
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 784)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
```

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  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .784
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DI043YO10"
                     /clone_lib="LTI_NFL006_PL2"
                     /tissue_type="placenta"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer.  Five prime end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      234 a    135 c    126 g    285 t      4 others
ORIGIN


  Query Match             28.3%;  Score 768.2;  DB 10;  Length 784;
  Best Local Similarity   99.4%;  Pred. No. 9.2e-115;
  Matches  778;  Conservative    3;  Mismatches    1;  Indels    1;  Gaps    1;

Qy   1830 ggaatgcattcttgacatttccgaacacacattaagtgaaaatgacttagaagaactaag 1889
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    784 GGAATGCATTCTTGACATTTCCGAACACACATTAAGTGAAAATGACTTAGAAGAACTAAG 725

Qy   1890 ggtagatcactataaatgtaacatacaggcatctgtacatgtttctgatttcagtacaga 1949
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    724 GGTAGATCACTATAAATGTAACATACAGGCATCTGTACATGTTTCTGATTTCAGTACAGA 665

Qy   1950 taatagtggatctcaaccaaaacagaagt-cagatactgtgctttttccagcaaaggatc 2008
           |||||||||||||||||| |||||||| ||||||||||||||||||||||||||||||
Db    664 TAATAGTGGATCTCAACCAACACAGAAGTGCAGATACTGTGCTTTTTCCAGCAAAGGATC 605

Qy   2009 tcaaggaaaaggaccttcattcaatatttactcatgattctggtctgataacaataaaca 2068
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    604 TCAAGGAAAAGGACCTTCATTCAATATTTACTCATGATTCTGGTCTGATAACAATAAACA 545

Qy   2069 gttcacaagagcacctaactgttcaggcaaaggctccattccatactcctcctgaggaac 2128
           ||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||||
Db    544 GTTCACAAGAGCACCTAACTGTTCAGGCAAAGGCYCCATTCCATACTCCTCCTGAGGAAC 485

Qy   2129 ccaatgaatgtgacttcaagaatatggatagtttaccttctggtaaaatacatcgaaaag 2188
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    484 CCAATGAATGTGACTTCAAGAATATGGATAGTTTACCTTCTGGTAAAATACATCGAAAAG 425

Qy   2189 tgaaaataatattaggacgaaatagaaaagaaaatctggaaccaaatgctgaatttgata 2248
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    424 TGAAAATAATATTAGGACGAAATAGAAAAGAAAATCTGGAACCAAATGCTGAATTTGATA 365

Qy   2249 aaagaactgaatttattacacaagaagaaaacagaatttgtagttcaccggtacagtctt 2308
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    364 AAAGAACTGAATTTATTACACAAGAAGAAAACAGAATTTGTAGTTCACCGGTACAGTCTT 305

Qy   2309 tactagacttgtttcagactagtgaagagaaatcagaatttttgggtttcacaagctaca 2368
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    304 TACTAGACTTGTTTCAGACTAGTGAAGAGAAATCAGAATTTTTGGGTTTCACAAGCTACA 245

Qy   2369 cagaaaagagtggtatatgcaatgttttagatatttgggaagaggaaaattcagataatc 2428
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    244 CAGAAAAGAGTGGTATATGCAATGTTTTAGATATTTGGGAAGAGGAAAATTCAGATAATC 185

Qy   2429 tgttaacagcgtttttctcgtccccttcaacttctacatttactggcttttagaatttaa 2488
           ||||||||||||||||||||||||||||||||||:|||||||||||||||||||||:|
Db    184 TGTTAACAGCGTTTTTCTCGTCCCCTTCAACTTCTACATTKACTGGCTTTTAGAATTTRA 125
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Qy   2489 aaaatgcatacttttcagaagtgataaggatcatattcttgaaatttttataaatatgta 2548
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    124 AAAATGCATACTTTTCAGAAGTGATAAGGATCATATTCTTGAAATTTTTATAAATATGTA 65

Qy   2549 tggaaattcttaggatttttttaccagctttgtttacagacccaaatgtaaatattaaaa 2608
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     64 TGGAAATTCTTAGGATTTTTTTACCAGCTTTGTTTACAGACCCAAATGTAAATATTAAAA 5

Qy   2609 ata 2611
           |||
Db      4 ATA 2


RESULT   5
BG720949
LOCUS       BG720949     1019 bp    mRNA            EST       08-MAY-2001
DEFINITION  602692613F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4825034 5',
            mRNA sequence.
ACCESSION   BG720949
VERSION     BG720949.1  GI:14000136
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1019)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10737  row: i  column: 03
            High quality sequence stop: 785.
FEATURES             Location/Qualifiers
     source          1. .1019
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4825034"
                     /clone_lib="NIH_MGC_97"
                     /lab_host="DH10B"
                     /note="Organ: testis; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTTVN-3',
                     size-selected for  average insert size 2.2 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for full-length clones and constructed using the
                     Cap-trapper method (Carninci, in preparation).  Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      320 a    221 c    248 g    230 t
ORIGIN


  Query Match             27.7%;  Score 753.4;  DB 11;  Length 1019;
  Best Local Similarity   96.3%;  Pred. No. 2.2e-112;
  Matches  814;  Conservative    0;  Mismatches   26;  Indels    5;  Gaps    4;

Qy    337 ggagccggatccggccccggaaacccgacctgcagacgcggtacctctactgcgtagagg 396
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      5 GGAGCCGGATCCGGCCCCGGAAACCCGACCTGCAGACGCGGTACCTCTACTGCGTAGAGG 64

Qy    397 ccgtagctggcggaaggagagaggcggccgtcctgtcaacaggccgggggaagccgtgct 456
           |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db     65 CCGTAGCTGGCGGAAGGAGAGAGGCGGCCGTCCTGTCAACAGACCGGGGGAAGCCGTGCT 124
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Qy     457 ttcgcggctgcccggtgcgacactttctccggacccagcatgtaggtgccgggcgactgc 516
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     125 TTCGCGGCTGCCCGGTGCGACACTTTCTCCGGACCCAGCATGTAGGTGCCGGGCGACTGC 184

Qy     517 catgaactccggagccatgaggatccacagtaaaggacatttccagggtggaatccaagt 576
           |||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db     185 CATGAACTCCGGAGCCATGAGGATCCACAGTAAAGGACATTTCCA-GGTGGAATCCAAGT 243

Qy     577 caaaaatgaaaaaaacagaccatctctgaaatctctgaaaactgataacaggccagaaaa 636
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     244 CAAAAATGAAAAAAACAGACCATCTCTGAAATCTCTGAAAACTGATAACAGGCCAGAAAA 303

Qy     637 atccaaatgtaagccactttggggaaaagtattttaccttgacttaccttctgtcaccat 696
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Db     304 ATCCAAATGTAAGCCACTTTGGGGAAAAGTATTTTACCTTGACTTACCTTCTGTCACCAT 363

Qy     697 atctgaaaaacttcaaaaggacattaaggatctgggagggcgagttgaagaatttctcag 756
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     364 ATCTGAAAAACTTCAAAAGGACATTAAGGATCTGGGAGGGCGAGTTGAAGAATTTCTCAG 423

Qy     757 caaagatatcagttatcttatttca--aataagaaggaagctaaatttgcacaaaccttg 814
           |||||||||||||||||||||||||  |  | | ||||||||||||||||||||||||||
Db     424 CAAAGATATCAGTTATCTTATTTCAACATAAGAACGGAAGCTAAATTTGCACAAACCTTG 483

Qy     815 ggtcgaatttctcctgtaccaagtccagaatctgcatatactgcagaaaccacttcacct 874
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     484 GGTCGAATTTCTCCTGTACCAAGTCCAGAATCTGCATATACTGCAGAAACCACTTCACCT 543

Qy     875 catcccagccatgatggaagttcatttaagtcaccagacacagtgtgtttaagcagagga 934
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     544 CATCCCAGCCATGATGGAAGTTCATTTAAGTCACCAGACACAGTGTGTTTAAGCAGAGGA 603

Qy     935 aaattattagttgaaaaagctatcaaggaccatgattttattccttcaaatagtatatta 994
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     604 AAATTATTAGTTGAAAAAGCTATCAAGGACCATGATTTTATTCCTTCAAATAGTATATTA 663

Qy     995 tcaaatgccttgtcatggggagtaaaaattcttcatattgatgaca-ttagatactacat 1053
           |||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||
Db     664 TCAAATGCCTTGTCATGGGGAGTAAAAATTCTTCATATTGATGACACTTAGATACTACAT 723

Qy    1054 tgaacaaaagaaaaaagagttgtatttactcaagaaatcaagtac-ttcagtaagagatg 1112
           |||||||||||||||||||||||||||||||||||||||||||| ||||||    |||
Db     724 TGAACAAAAGAAAAAAGAGTTGTATTTACTCAAGAAATCAAGTACTTTCAGTAGAGAATG 783

Qy    1113 ggggcaaaagagttggtagtggtgcacaaaaaacaagaacaggaagactcaaaaagcctt 1172
           ||||||||||| |||||||||||   |||| |||  | | |||  ||||| | ||||||
Db     784 GGGGCAAAAGAAGTGGTAGTGGTGGCAAAAACACAGCACCGGGAGAACTCAGAGAGCCTT 843

Qy    1173 ttgta 1177
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Db     844 GGGTA 848


RESULT   6
AL559244
LOCUS       AL559244      725 bp    mRNA            EST       16-FEB-2001
DEFINITION  AL559244 LTI_NFL008_TC2 Homo sapiens cDNA clone CS0DJ012YL06 5
            prime, mRNA sequence.
ACCESSION   AL559244
VERSION     AL559244.1  GI:12904555
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 725)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1. .725
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                     /db_xref="taxon:9606"
                     /clone="CS0DJ012YL06"
                     /clone_lib="LTI_NFL008_TC2"
                     /sex="male"
                     /tissue_type="T cells from T cell leukemia"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime  end
                     enriched, double-stranded cDNA was digested with Not I and
                     cloned into the Not I and Eco RV sites of the pCMVSPORT 6
                     vector. Library was normalized. Library was constructed by
                     Life Technologies. Contact : Feng Liang Life Technologies,
                     a division of Invitrogen 9800 Medical Center Drive
                     Rockville, Maryland 20850, USA Fax : (1) 301 610 8371
                     Email : fliang@lifetech.com URL :
                     http://fulllength.invitrogen.com"
BASE COUNT      224 a    166 c    164 g    171 t
ORIGIN


  Query Match           26.6%;  Score 723.4;  DB 10;  Length 725;
  Best Local Similarity   99.9%;  Pred. No. 1.6e-107;
  Matches  724;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     329 cgcgccttggagccggatccggccccggaaacccgacctgcagacgcggtacctctactg 388
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1 CGCGCCTTGGAGCCGGATCCGGCCCCGGAAACCCGACCTGCAGACGCGGTACCTCTACTG 60

Qy     389 cgtagaggccgtagctggcggaaggagagaggcggccgtcctgtcaacaggccgggggaa 448
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      61 CGTAGAGGCCGTAGCTGGCGGAAGGAGAGAGGCGGCCGTCCTGTCAACAGGCCGGGGGAA 120

Qy     449 gccgtgctttcgcggctgcccggtgcgacactttctccggacccagcatgtaggtgccgg 508
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     121 GCCGTGCTTTCGCGGCTGCCCGGTGCGACACTTTCTCCGGACCCAGCATGTAGGTGCCGG 180

Qy     509 gcgactgccatgaactccggagccatgaggatccacagtaaaggacatttccagggtgga 568
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     181 GCGACTGCCATGAACTCCGGAGCCATGAGGATCCACAGTAAAGGACATTTCCAGGGTGGA 240

Qy     569 atccaagtcaaaaatgaaaaaaacagaccatctctgaaatctctgaaaactgataacagg 628
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     241 ATCCAAGTCAAAAATGAAAAAAACAGACCATCTCTGAAATCTCTGAAAACTGATAACAGG 300

Qy     629 ccagaaaaatccaaatgtaagccactttggggaaaagtattttaccttgacttaccttct 688
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Db     301 CCAGAAAAATCCAAATGTAAGCCACTTTGGGGAAAAGTATTTTACCTTGACTTACCTTCT 360

Qy     689 gtcaccatatctgaaaaacttcaaaaggacattaaggatctgggagggcgagttgaagaa 748
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Db     361 GTCACCATATCTGAAAAACTTCAAAAGGACATTAAGGATCTGGGAGGGCGAGTTGAAGAA 420

Qy     749 tttctcagcaaagatatcagttatcttatttcaaatagaaggaagctaaatttgcacaa 808
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     421 TTTCTCAGCAAAGATATCAGTTATCTTATTTCAAATAAGAAGGAAGCTAAATTTGCACAA 480

Qy     809 accttgggtcgaatttctcctgtaccaagtccagaatctgcatatactgcagaaaccact 868
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Db     481 ACCTTGGGTCGAATTTCTCCTGTACCAAGTCCAGAATCTACATATACTGCAGAAACCACT 540

Qy     869 tcacctcatcccagccatgatggaagttcatttaagtcaccagacacagtgtgtttaagc 928
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Db     541 TCACCTCATCCCAGCCATGATGGAAGTTCATTTAAGTCACCAGACACAGTGTGTTTAAGC 600

Qy     929 agaggaaaattattagttgaaaaagctatcaaggaccatgattttattccttcaaatagt 988
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     601 AGAGGAAAATTATTAGTTGAAAAAGCTATCAAGGACCATGATTTTATTCCTTCAAATAGT 660

Qy     989 atattatcaaatgccttgtcatggggagtaaaaattcttcatattgatgacattagatac 1048
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Db    661 ATATTATCAAATGCCTTGTCATGGGGAGTAAAAATTCTTCATATTGATGACATTAGATAC 720

Qy   1049 tacat 1053
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Db    721 TACAT 725


RESULT   7
AU128881
LOCUS       AU128881      903 bp    mRNA            EST       24-OCT-2000
DEFINITION  AU128881 NT2RP2 Homo sapiens cDNA clone NT2RP2004396 5', mRNA
            sequence.
ACCESSION   AU128881
VERSION     AU128881.1  GI:10989235
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 903)
  AUTHORS   Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
            Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
            Isogai,T.
  TITLE     HRI human cDNA project
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Takao Isogai
            Genomics Laboratory
            Helix Research Institute
            1532-3 Yana, Kisarazu, Chiba 292-0812, Japan
            Tel: 81-438-52-3951
            Fax: 81-438-52-3952
            Email: genomics@hri.co.jp
            HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
            Research Institute; cDNA library construction: Department of
            Virology, Institute of Medical Science, University of Tokyo, and
            Helix Research Institute.
FEATURES             Location/Qualifiers
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                     /clone_lib="NT2RP2"
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                     /cell_line="NT2"
                     /note="Vector: pME18SFL3; mRNA from NT2 neuronal precursor
                     cells after 2-weeks retinoic acid (RA) induction"
BASE COUNT      326 a    165 c    157 g    242 t     13 others
ORIGIN


  Query Match           26.5%;  Score 721.6;  DB 10;  Length 903;
  Best Local Similarity   92.3%;  Pred. No. 3e-107;
  Matches  820;  Conservative    0;  Mismatches   56;  Indels   12;  Gaps    6;

Qy   1593 tatttctcagaaagattgccaggaagatgatacaacagt-gaaggagcagaatttcctgt 1651
           |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||
Db      1 TATTTCTCAGAAAGATTGCCAGGAAGATGATACAACAGTGGAAGGAGCAGAATTTCCTGT 60

Qy   1652 ataaagagacccaggaaactgaaaaaaagctcctgtttatttcagagcccatccccccacc 1711
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ATAAAGAGACCCAGGAAACTGAAAAAAAGCTCCTGTTTATTTCAGAGCCCATCCCCCACC 120

Qy   1712 cttcaaatgaattgagagggcttaatgagaaaatgagtaataaatgttccatgttaagta 1771
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 CTTCAAATGAATTGAGAGGGCTTAATGAGAAAATGAGTAATAAATGTTCCATGTTAAGTA 180

Qy   1772 cagctgaagatgacataagacagaattttacacagctacctctacataaaaacaaacagg 1831
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Db    181 CAGCTGAAGATGACATAAGACAGAATTTTACACAGCTACCTCTACATAAAAACAAACAGG 240

Qy   1832 aatgcattcttgacatttccgaacacacattaagtgaaaatgacttagaagaactaaggg 1891
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||| |||
Db    241 AATGCATTCTTGACATTTCCGAACACACATTAAGTGAAAATGACTTAGAAGAACTANGGG 300
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Qy   1892 tagatcactataaaatgtaacatacaggcatctgtacatgtttctgatttcagtacagata 1951
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Db    301 TAGATCACTATAAATGTAACATACAGGCATCTGTACATGTTTCTGATTTCAGTACAGATA 360

Qy   1952 atagtggatctcaaccaaaacagaagtcagatactgtgctttttccagcaaaggatctca 2011
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 ATAGTGGATCTCAACCAAAACAGAAGTCAGATACTGTGCTTTTTCCAGCAAAGGATCTCA 420

Qy   2012 aggaaaaggaccttcattcaatatttactcatgattctggtctgataacaataaacagtt 2071
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 AGGAAAAGGACCTTCATTCAATATTTACTCATGATTCTGGTCTGATAACAATAAACAGTT 480

Qy   2072 cacaagagcacctaactgttcaggcaaaggctccattccatactcctcctgaggaaccca 2131
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Db    481 CACAAGAGCACCTAACTGTTCAGGCNAAGGCTCCATTCCATACTCCTCCTGAGGAACCCA 540

Qy   2132 atgaatgtgacttcaagaatatggatagtttaccttctggtaaaatacatcgaaaagtga 2191
          |||||||||||||||||||||||||||||||||||| |||||| ||||||||||||||||||
Db    541 ATGAATGTGACTTCAAGAATATGGATAGTTTACCCTCTGGTNAAATACATCGAAAAGTGA 600

Qy   2192 aaataatatta-ggacgaaatagaaaagaaaatctggaaccaaatgctgaatttgataaa 2250
          |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db    601 AAATAATATTAGGGACGAAATAGAAAAGAAAATCTGGAACCAAATGCTGAATTTGATAAA 660

Qy   2251 agaactgaatttattacacaagaagaaaacagaatttgtagttcaccggtacagtctttta 2310
          |||||||||||||| | | |||||||||| |||||||  ||||||||||||||||||||
Db    661 AGAACTGAATTTATTNCCCCAGAAGAAAACNGAATTTGT-TTTCACCGGTACAGTCTTTA 719

Qy   2311 ctagacttgtttcagactagtgaagagaaatcagaatttttgggtttcacaagctacaca 2370
          ||| ||| || ||| | ||||| |||||||||||||||| |||||||| ||
Db    720 CTANACTGTTTCAGACTAGTGGAAAAAAAAATCNGAATTTTTGGGTTTCNCAAGCTACCCA 779

Qy   2371 gaaaa--gagtggtatatgcaatgttttagatatttggg-----aagaggaaaattcaga 2423
          |||||  | |||||||||| |||||||  | || | ||     ||||  ||     |
Db    780 GAAAAAGAATTGGTATATGCCATGTTTTTAANATATTGGGGAAAAAGAAAAATTCCNAAT 839

Qy   2424 taatctgttaacagcgtttttt--ctcgtccccttcaacttctacattt 2469
            |    ||||||||||||||  |  ||||| | |||||||| |  ||
Db    840 AATCTGGTTAACAGCGTTTTTTCCCNGTCCCTTCCAACTTCTTCCNTT 887


RESULT   8
AL580899/c
LOCUS       AL580899      742 bp    mRNA            EST       16-FEB-2001
DEFINITION  AL580899 LTI_NFL008_TC2 Homo sapiens cDNA clone CS0DJ012YL06 3
            prime, mRNA sequence.
ACCESSION   AL580899
VERSION     AL580899.1  GI:12947367
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 742)
  AUTHORS   Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
  TITLE     Full-length cDNA libraries and normalization
  JOURNAL   Unpublished (2001)
COMMENT     Contact: Genoscope
            Genoscope - Centre National de Sequencage
            BP 191 91006 EVRY cedex - France
            Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr.
FEATURES             Location/Qualifiers
     source          1..742
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="CS0DJ012YL06"
                     /clone_lib="LTI_NFL008_TC2"
                     /sex="male"
                     /tissue_type="T cells from T cell leukemia"
                     /note="Vector: pCMVSPORT 6; Site_1: NotI; 1st strand cDNA
                     was primed with a NotI-oligo(dT) primer. Five prime  end
                     enriched, double-stranded cDNA was digested with Not I and
```

cloned into the Not I and Eco RV sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies. Contact : Feng Liang Life Technologies, a division of Invitrogen 9800 Medical Center Drive Rockville, Maryland 20850, USA Fax : (1) 301 610 8371 Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com"
BASE COUNT 228 a 124 c 120 g 269 t 1 others
ORIGIN

Query Match 26.4%; Score 719; DB 10; Length 742;
Best Local Similarity 99.1%; Pred. No. 8.3e-107;
Matches 734; Conservative 0; Mismatches 5; Indels 2; Gaps 1;

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Qy   1912 atacaggcatctgtacatgtttctgatttcagtacagataatagtggatctcaaccaaaa 1971
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    742 ATACAGGCATCTGTACATGTTTCTGATTTCAGTACAGATAATAGTGGATCTCAACCAAAA 683

Qy   1972 cagaagtcagatactgtgctttttccagcaaaggatctcaaggaaaaggaccttcattca 2031
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    682 CAGAAGTCAGATACTGTGCTTTTTCCAGCAAAGGATCTCAAGGAAAAGGACCTTCATTCA 623

Qy   2032 atatttactcatgattctggtctgataacaataaacagttcacaagagcacctaactgtt 2091
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    622 ATATTTACTCATGATTCTGGTCTGATAACAATAAACAGTTCACAAGAGCACCTAACTGTT 563

Qy   2092 caggcaaaggctccattccatactcctcctgaggaacccaatgaatgtgacttcaagaat 2151
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    562 CAGGCAAAGGCTCCATTCCATACTCCTCCTGAGGAACCCAATGAATGTGACTTCAAGAAT 503

Qy   2152 atggatagtttaccttctggtaaaatacatcgaaaagtgaaaataatattaggacgaaat 2211
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    502 ATGGATAGTTTACCTTCTGGTAAAATACATCGAAAAGTGAAAATAATATTAGGACGAAAT 443

Qy   2212 agaaaagaaaatctggaaccaaatgctgaatttgataaaagaactgaatttattacacaa 2271
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    442 AGAAAAGAAAATCTGGAACCAAATGCTGAATTTGATAAAAGAACTGAATTTATTACACAA 383

Qy   2272 gaagaaaacagaatttgtagttcaccggtacagtctttactagacttgtttcagactagt 2331
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    382 GAAGAAAACAGAATTTGTAGTTCACCGGTACAGTCTTTACTAGACTTGTTTCAGACTAGT 323

Qy   2332 gaagagaaatcagaatttttgggtttcacaagctacacagaaaagagtggtatatgcaat 2391
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    322 GAAGAGAAATCAGAATTTTTGGGTTTCACAAGCTACACAGAAAAGAGTGGTATATGCAAT 263

Qy   2392 gttttagatatttgggaagaggaaaattcag--ataatctgttaacagcgtttttctcgt 2449
          |||||||||||||||||||||||||||||     ||||||||||||||||||||||||
Db    262 GTTTTAGATATTTGGGAAGAGGAAAATTCAGCATACATCTGTTAACAGCGTTTTTCTCGT 203

Qy   2450 ccccttcaacttctacatttactggctttagaatttaaaaaatgcatacttttcagaag 2509
          |||||||||||||||||| |||||||||||||| ||||||||||||||||||||||||
Db    202 CCCCTTCAACTTCTACATTGACTGGCTTTTAGAATCTAAAAAATGCATACTTTTCAGAAG 143

Qy   2510 tgataaggatcatattcttgaaatttttataaatatgtatggaaattcttaggatttttt 2569
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    142 TGATAAGGATCATATTCTTGAAATTTTTATAAATATGTATGGAAATTCTTAGGATTTTTT 83

Qy   2570 taccagctttgtttacagacccaaatgtaaatattaaaaataaatatttgcaatttttcta 2629
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     82 TACCAGCTTTGTTTACAGACCCAAATGTAAATATTAAAAATAAATATTTGCAATTTTCTA 23

Qy   2630 cagaattgaatacctgttaaa 2650
          ||||||||||||||||||||
Db     22 CAGAATTGAATACCTGTTAAA 2
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RESULT 9
AI948485/c
LOCUS AI948485 744 bp mRNA EST 08-MAR-2000
DEFINITION wq06d08.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2470479 3' similar to TR:O75226 O75226 WUGSC:H_RG135C18.1 PROTEIN ;, mRNA sequence.
ACCESSION AI948485
VERSION AI948485.1 GI:5740795
KEYWORDS EST.
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 744)
AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL Unpublished (1997)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 1484 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 432.
FEATURES Location/Qualifiers
source 1. .744
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:2470479"
/clone_lib="NCI_CGAP_Kid12"
/tissue_type="2 pooled tumors (clear cell type)"
/lab_host="DH10B"
/note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; Plasmid DNA from the normalized library NCI_CGAP_Kid5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1323912-1325831, 1471368-1472903 and 1492104-1493255). Subtraction by Bento Soares and M. Fatima Bonaldo. "
BASE COUNT 223 a 127 c 117 g 277 t
ORIGIN

Query Match 26.1%; Score 710; DB 10; Length 744;
Best Local Similarity 97.3%; Pred. No. 2.4e-105;
Matches 722; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

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Qy   1900 tataaatgtaacatacaggcatctgtacatgtttctgatttcagtacagataatagtgga 1959
          ||| |||||||||| |||||| || ||||||||||||||| |||||||||| ||||||||
Db    744 TATCAATGTAACAAACAGGCGTCGGTACATGTTTCTGATCTCAGTACAGATCATAGTGGA 685

Qy   1960 tctcaaccaaaaacagaagtcagatactgtgctttttccagcaaaggatctcaaggaaaag 2019
          ||||||||| | ||||||||||||||||||||||||||||||||||||||||||| ||
Db    684 TCTCAACCAGAGCAGAAGTCAGATACTGTGCTTTTTCCAGCAAAGGATCTCAAGGAACAG 625

Qy   2020 gaccttcattcaatatttactcatgattctggtctgataacaataaacagttcacaagag 2079
          |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db    624 GACCTTCATTCGATATTTACTCATGATTCTGGTCTGATAACAATAAACAGTTCACAAGAG 565

Qy   2080 cacctaactgttcaggcaaaggctccattccatactcctcctgaggaacccaatgaatgt 2139
          |||||||||||||||||||||||||||||||||||||||| ||||||||||||||||||
Db    564 CACCTAACTGTTCAGGCAAAGGCTCCATTCCATACTCCTCGTGAGGAACCCAATGAATGT 505

Qy   2140 gacttcaagaatatggatagtttaccttctggtaaaatacatcgaaaagtgaaaataata 2199
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    504 GACTTCAAGAATATGGATAGTTTACCTTCTGGTAAAATACATCGAAAAGTGAAAATAATA 445

Qy   2200 ttaggacgaaatagaaaagaaaatctggaaccaaatgctgaatttgataaaagaactgaa 2259
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          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    444 TTAGGACGAAATAGAAAAGAAAATCTGGAACCAAATGCTGAATTTGATAAAAGAACTGAA 385

Qy   2260 tttattacacaagaagaaaacagaatttgtagttcaccggtacagtctttactagacttg 2319
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    384 TTTATTACACAAGAAGAAAACAGAATTTGTAGTTCACCGGTACAGTCTTTACTAGACTTG 325

Qy   2320 tttcagactagtgaagagaaatcagaatttttgggtttcacaagctacacagaaaagagt 2379
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    324 TTTCAGACTAGTGAAGAGAAATCAGAATTTTTGGGTTTCACAAGCTACACAGAAAAGAGT 265

Qy   2380 ggtatatgcaatgttttagatatttgggaagaggaaaattcagataatctgttaacagcg 2439
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    264 GGTATATGCAATGTTTTAGATATTTGGGAAGAGGAAAATTCAGATAATCTGTTAACAGCG 205

Qy   2440 tttttctcgtccccttcaacttctacatttactggcttttagaatttaaaaaatgcatac 2499
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    204 TTTTTCTCGTCCCCTTCAACTTCTACATTTACTGGCTTTTAGAATTTAAAAAATGCATAC 145

Qy   2500 ttttcagaagtgataaggatcatattcttgaaatttttataaatatgtatggaaatttctt 2559
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    144 TTTTCAGAAGTGATAAGGATCATATTCTTGAAATTTTTATAAATATGTATGGAAATTCTT 85

Qy   2560 aggatttttttaccagctttgtttacagacccaaatgtaaatattaaaaataaatatttg 2619
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     84 AGGATTTTTTTACCAGCTTTGTTTACAGACCCAAATGTAAATATTAAAAATAAATATTTG 25

Qy   2620 caatttttctacagaattgaata 2641
            ||  ||||| | ||   || |
Db     24 AAAAATTCTAAAAAAAAAAAA 3


RESULT  10
BG496289
LOCUS       BG496289      821 bp    mRNA            EST       27-MAR-2001
DEFINITION  602538259F1 NIH_MGC_59 Homo sapiens cDNA clone IMAGE:4659446 5',
            mRNA sequence.
ACCESSION   BG496289
VERSION     BG496289.1  GI:13457805
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 821)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1455  row: e  column: 15
            High quality sequence stop: 742.
FEATURES             Location/Qualifiers
     source          1. .821
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4659446"
                     /clone_lib="NIH_MGC_59"
                     /tissue_type="mucoepidermoid carcinoma"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /note="Organ: lung; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc);
                     Double-stranded cDNA was prepared from cell line RNA.  5'
                     and 3' adaptors were used in cloning as follows: 5'
                     adaptor sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor
                     sequence:  5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'
                     (where B = A, C, or G and N = A, C,  G, or T).  Average
                     insert size 1.65 kb (range 0.9-4.0 kb). 15/15 colonies
                     contained  inserts by PCR. This library was enriched for
                     full-length clones and was constructed by Clontech
                     Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                     Library."
BASE COUNT      273 a    166 c    176 g    206 t
ORIGIN


  Query Match             25.6%;  Score 696.4;  DB 11;  Length 821;
  Best Local Similarity   97.2%;  Pred. No. 3.7e-103;
  Matches  762;  Conservative    0;  Mismatches   16;  Indels    6;  Gaps    5;

Qy    417 gaggcggccgtcctgtcaacaggccgggggaagccgtgctttcgcggctgcccggtgcga 476
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      1 GAGGCGGCCGTCCTGTCAACAGGCCGGGGGAAGCCGTGCTTTCGCGGCTGCCCGGTGCGA 60

Qy    477 cactttctccggacccagcatgtaggtgccgggcgactgccatgaactccggagccatga 536
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 CACTTTCTCCGGACCCAGCATGTAGGTGCCGGGCGACTGCCATGAACTCCGGAGCCATGA 120

Qy    537 ggatccacagtaaaggacatttccagggtggaatccaagtcaaaaatgaaaaaaacagac 596
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 GGATCCACAGTAAAGGACATTTCCAGGGTGGAATCCAAGTCAAAAATGAAAAAAACAGAC 180

Qy    597 catctctgaaatctctgaaaactgataacaggccagaaaaatccaaatgtaagccacttt 656
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CATCTCTGAAATCTCTGAAAACTGATAACAGGCCAGAAAAATCCAAATGTAAGCCACTTT 240

Qy    657 ggggaaaagtattttaccttgacttaccttctgtcaccatatctgaaaaacttcaaaagg 716
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 GGGGAAAAGTATTTTACCTTGACTTACCTTCTGTCACCATATCTGAAAAACTTCAAAAGG 300

Qy    717 acattaaggatctgggagggcgagttgaagaatttctcagcaaagatatcagttatctta 776
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    301 ACATTAAGGATCTGGGAGGGCGAGTTGAAGAATTTCTCAGCAAAGATATCAGTTATCTTA 360

Qy    777 tttcaaataagaaggaagctaaatttgcacaaaccttgggtcgaatttctcctgtaccaa 836
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    361 TTTCAAATAAGAAGGAAGCTAAATTTGCACAAACCTTGGGTCGAATTTCTCCTGTACCAA 420

Qy    837 gtccagaatctgcatatactgcagaaaccacttcacctcatcccagccatgatggaagtt 896
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 GTCCAGAATCTGCATATACTGCAGAAACCACTTCACCTCATCCCAGCCATGATGGAAGTT 480

Qy    897 catttaagtcaccagacacagtgtgtttaagcagaggaaaattattagttgaaaaagcta 956
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    481 CATTTAAGTCACCAGACACAGTGTGTTTAAGCAGAGGAAAATTATTAGTTGAAAAAGCTA 540

Qy    957 tcaaggaccatgattttattccttcaaatagtatattatcaaatgcc-ttgtcatgggga 1015
          |||||||||||||||||||||||||||||||||||||||||||||| |||||||||||||
Db    541 TCAAGGACCATGATTTTATTCCTTCAAATAGTATATTATCAAATGCCTTTGTCATGGGGA 600

Qy   1016 gtaaaaattcttcatattgatga-cattagatactacattgaacaaaagaaaaaagagttt 1074
          |||||||||||||||||||||| | |||||||||||||||||| |||||| |||||||
Db    601 GTAAAAATTCTTCATATTGATGACCTTTAGATACTACATTGAAC-AAAGAACAAAGAGTG 659

Qy   1075 gtatttactcaagaaatcaagtacttcagtaagagatgggggcaaaagagttggtagtgg 1134
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    660 GTATTTACTCAAGAAATCAAGTACTTCAGTAAGAGATGGGGGCAAA--GAGTGGTAGTGG 717

Qy   1135 tgcacaaaaaacaagaacaggaagactcaaaaagccttttgtaaaggtggaagatatgag 1194
          |||||||||||||||||  | |       |||||||||||||| ||||||| |||||||||
Db    718 TGCACAAAAAACAAGAACCAGGAAGACTCAAAAGCCTTTTGT-AAGGTGGCAGATATGAG 776

Qy   1195 ccaa 1198
          ||||
Db    777 CCAA 780


RESULT  11
BG716928
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LOCUS       BG716928      703 bp    mRNA            EST       08-MAY-2001
DEFINITION  602689445F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4821970 5',
            mRNA sequence.
ACCESSION   BG716928
VERSION     BG716928.1  GI:13996115
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 703)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10729  row: i  column: 11
            High quality sequence stop: 703.
FEATURES             Location/Qualifiers
     source          1. .703
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4821970"
                     /clone_lib="NIH_MGC_97"
                     /lab_host="DH10B"
                     /note="Organ: testis; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3',
                     size-selected for  average insert size 2.2 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for full-length clones and constructed using the
                     Cap-trapper method (Carninci, in preparation).  Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      199 a    178 c    169 g    157 t
ORIGIN
```

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  Query Match             25.5%;  Score 692.4;  DB 11;  Length 703;
  Best Local Similarity   99.9%;  Pred. No. 1.7e-102;
  Matches  693;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy     269 cgcgttttcaaatcttcaaccgccgcagcccactcgtttgtgctttgcgccttcctcctc 328
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       9 CGCGTTTTCAAATCTTCAACCGCCGCAGCCCACTCGTTTGTGCTTTGCGCCTTCCTCCTC 68

Qy     329 cgcgccttggagccggatccggccccggaaacccgacctgcagacgcggtacctctactg 388
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      69 CGCGCCTTGGAGCCGGATCCGGCCCCGGAAACCCGACCTGCAGACGCGGTACCTCTACTG 128

Qy     389 cgtagaggccgtagctggcggaaggagagaggcggccgtcctgtcaacaggccgggggaa 448
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     129 CGTAGAGGCCGTAGCTGGCGGAAGGAGAGAGGCGGCCGTCCTGTCAACAGGCCGGGGGAA 188

Qy     449 gccgtgctttcgcggctgcccggtgcgacactttctccggacccagcatgtaggtgccgg 508
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     189 GCCGTGCTTTCGCGGCTGCCCGGTGCGACACTTTCTCCGGACCCAGCATGTAGGTGCCGG 248

Qy     509 gcgactgccatgaactccggagccatgaggatccacagtaaaggacatttccagggtgga 568
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     249 GCGACTGCCATGAACTCCGGAGCCATGAGGATCCACAGTAAAGGACATTTCCAGGGTGGA 308

Qy     569 atccaagtcaaaaatgaaaaaaacagaccatctctgaaatctctgaaaactgataacagg 628
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     309 ATCCAAGTCAAAAATGAAAAAAACAGACCATCTCTGAAATCTCTGAAAACTGATAACAGG 368

Qy     629 ccagaaaaatccaaatgtaagccactttggggaaaagtattttaccttgacttaccttct 688
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     369 CCAGAAAAATCCAAATGTAAGCCACTTTGGGGAAAAGTATTTTACCTTGACTTACCTTCT 428

Qy     689 gtcaccatatctgaaaaacttcaaaaggacattaaggatctgggagggcgagttgaagaa 748
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     429 GTCACCATATCTGAAAAACTTCAAAAGGACATTAAGGATCTGGGAGGGCGAGTTGAAGAA 488

Qy     749 tttctcagcaaagatatcagttatcttatttcaaataagaaggaagctaaatttgcacaa 808
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     489 TTTCTCAGCAAAGATATCAGTTATCTTATTTCAAATAAGAAGGAAGCTAAATTTGCACAA 548

Qy     809 accttgggtcgaatttctcctgtaccaagtccagaatctgcatatactgcagaaaccact 868
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     549 ACCTTGGGTCGAATTTCTCCTGTACCAAGTCCAGAATCTGCATATACTGCAGAAACCACT 608

Qy     869 tcacctcatcccagccatgatggaagttcatttaagtcaccagacacagtgtgtttaagc 928
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     609 TCACCTCATCCCAGCCATGATGGAAGTTCATTTAAGTCACCAGACACAGTGTGTTTAAGC 668

Qy     929 agaggaaaattattagttgaaaaagctatcaagg 962
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Db     669 AGAGGACAATTATTAGTTGAAAAAGCTATCAAGG 702
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RESULT  12
BG717397
LOCUS       BG717397      767 bp    mRNA            EST       08-MAY-2001
DEFINITION  602689740F1 NIH_MGC_97 Homo sapiens cDNA clone IMAGE:4822136 5',
            mRNA sequence.
ACCESSION   BG717397
VERSION     BG717397.1  GI:13996584
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 767)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
             cDNA Library Preparation: Michael J. Brownstein (NHGRI), Shiraki
            Toshiyuki and Piero Carninci (RIKEN)
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM10729  row: p  column: 09
            High quality sequence stop: 767.
FEATURES             Location/Qualifiers
     source          1. .767
                     /organism="Homo sapiens"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4822136"
                     /clone_lib="NIH_MGC_97"
                     /lab_host="DH10B"
                     /note="Organ: testis; Vector: pBluescriptR (modified
                     pBluescript KS+); Site_1: BamHI; Site_2: SalI-XhoI (gtcgag
                     ); Oligo-dT primed using primer 5'-TTTTTTTTTTTTTTTVN-3',
                     size-selected for  average insert size 2.2 kb and
                     normalized to ROT 5. This is a primary library enriched
                     for full-length clones and constructed using the
                     Cap-trapper method (Carninci, in preparation).  Library
                     constructed by M. Brownstein (NIMH/NHGRI, National
                     Institutes of Health). Note: this is a NIH_MGC Library."
BASE COUNT      215 a    193 c    185 g    174 t
ORIGIN
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  Query Match             25.4%;  Score 691.6;  DB 11;  Length 767;
  Best Local Similarity   98.2%;  Pred. No. 2.2e-102;
  Matches  752;  Conservative    0;  Mismatches    9;  Indels    5;  Gaps    5;

Qy    233 gggcggggcgcgcgtatcggcgccgcggccgcgtgacgcgttttcaaatcttcaaccgcc 292
          | | |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      2 GCGGGGGGTGCGCGTATCGGCGCCGCGGCCGCGTGACGCGTTTTCAAATCTTCAACCGCC 61

Qy    293 gcagcccactcgtttgtgctttgcgccttcctcctccgcgccttggagccggatccggcc 352
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     62 GCAGCCCACTCGTTTGTGCTTTGCGCCTTCCTCCTCCGCGCCTTGGAGCCGGATCCGGCC 121

Qy    353 ccggaaacccgacctgcagacgcggtacctctactgcgtagaggccgtagctggcggaag 412
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    122 CCGGAAACCCGACCTGCAGACGCGGTACCTCTACTGCGTAGAGGCCGTAGCTGGCGGAAG 181

Qy    413 gagagaggcggccgtcctgtcaacaggccgggggaagccgtgctttcgcggctgcccggt 472
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    182 GAGAGAGGCGGCCGTCCTGTCAACAGGCCGGGGGAAGCCGTGCTTTCGCGGCTGCCCGGT 241

Qy    473 gcgacactttctccggacccagcatgtaggtgccgggcgactgccatgaactccggagcc 532
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    242 GCGACACTTTCTCCGGACCCAGCATGTAGGTGCCGGGCGACTGCCATGAACTCCGGAGCC 301

Qy    533 atgaggatccacagtaaaggacatttccagggtggaatccaagtcaaaaatgaaaaaaac 592
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    302 ATGAGGATCCACAGTAAAGGACATTTCCAGGGTGGAATCCAAGTCAAAAATGAAAAAAAC 361

Qy    593 agaccatctctgaaatctctgaaaactgataacaggccagaaaaatccaaatgtaagcca 652
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    362 AGACCATCTCTGAAATCTCTGAAAACTGATAACAGGCCAGAAAAATCCAAATGTAAGCCA 421

Qy    653 ctttggggaaaagtattttaccttgacttaccttctgtcaccatatctgaaaaacttcaa 712
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    422 CTTTGGGGAAAAGTATTTTACCTTGACTTACCTTCTGTCACCATATCTGAAAAACTTCAA 481

Qy    713 aaggacattaaggatctgggagggcgagttgaaga-atttctcagcaaagatatcagtta 771
          |||||||||||||||||||||||||||||||||| |||||||||||||||||||||||||
Db    482 AAGGACATTAAGGATCTGGGAGGGCGAGTTGAAGACATTTCTCAGCAAAGATATCAGTTA 541

Qy    772 tcttatttcaaataagaaggaagctaaatttgcacaaaccttgggtcgaatttctcctgt 831
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    542 TCTTATTTCAAATAAGAAGGAAGCTAAATTTGCACAAACCTTGGGTCGAATTTCTCCTGT 601

Qy    832 accaagtccagaatctgcatatact-gcagaaaccacttcacctcatcccagccatgatg 890
          |||||||||||||||||||||||| |||||||||||||||||||||||| |||||||
Db    602 ACCAAGTCCAGAATCTGCATATACTGGCAGAAACCACTTCACCTCATCCCAG-CATGATG 660

Qy    891 gaagttcatttaagtcaccagacacagtgtgttt-aagcagaggaa-aattattagttga 948
          |||||||||||||||||||||||||||||||||| |||||||||| |||||||| |
Db    661 GAAGTTCATTTAAGTCACCAGACACAGTGTGTTTAAAGCAGAGGAACAATTATTACGTTG 720

Qy    949 aaaagctatcaaggaccatgattttattccttcaaatagtatatta 994
          ||||  ||||||||||||||||||||||||||||||||||||||
Db    721 AAAAAGTATCAAGGACCATGATTTTATTCCTTCAAATAGTATATTA 766


RESULT  13
BF793466
LOCUS       BF793466      712 bp    mRNA            EST       12-JAN-2001
DEFINITION  602254949F1 NIH_MGC_84 Homo sapiens cDNA clone IMAGE:4347156 5',
            mRNA sequence.
ACCESSION   BF793466
VERSION     BF793466.1  GI:12098520
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 712)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: Life Technologies, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM9970  row: a  column: 13
            High quality sequence stop: 712.
FEATURES             Location/Qualifiers
     source          1. .712
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:4347156"
                     /clone_lib="NIH_MGC_84"
                     /tissue_type="adrenal cortex carcinoma, cell line"
                     /lab_host="DH10B (phage-resistant)"
                     /note="Organ: adrenal gland; Vector: pCMV-SPORT6; Site_1:
                     NotI; Site_2: SalI; Cloned unidirectionally; oligo-dT
                     primed. Average insert size 1.229 kb. Library enriched for
                     full-length clones and constructed by Life Technologies.
                     Note: this is a NIH_MGC Library."
BASE COUNT      275 a    122 c    135 g    180 t
ORIGIN


  Query Match             25.2%;  Score 686;  DB 11;  Length 712;
  Best Local Similarity   100.0%;  Pred. No. 1.8e-101;
  Matches  686;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy   1198 aagccctgcagtccatttgatgtagacaagccatctagtatgcaaaagcaaactcaggtt 1257
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     27 AAGCCCTGCAGTCCATTTGATGTAGACAAGCCATCTAGTATGCAAAAGCAAACTCAGGTT 86

Qy   1258 aaactaagaatccaaacagatggcgataagtatggtggaacctcaattcaactccagttg 1317
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     87 AAACTAAGAATCCAAACAGATGGCGATAAGTATGGTGGAACCTCAATTCAACTCCAGTTG 146

Qy   1318 aaagagaagaagaaaaaaggatattgtgaatgttgcttgcagaaatatgaagatctagaa 1377
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    147 AAAGAGAAGAAGAAAAAAGGATATTGTGAATGTTGCTTGCAGAAATATGAAGATCTAGAA 206

Qy   1378 actcaccttctaagtgagcaacacagaaactttgcacagagtaaccagtatcaagttgtt 1437
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    207 ACTCACCTTCTAAGTGAGCAACACAGAAACTTTGCACAGAGTAACCAGTATCAAGTTGTT 266

Qy   1438 gatgatattgtatctaagttagtttttgactttgtggaatatgaaaaggacacacctaaa 1497
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    267 GATGATATTGTATCTAAGTTAGTTTTTGACTTTGTGGAATATGAAAAGGACACACCTAAA 326

Qy   1498 aagaaaagaataaaatacagtgttggatccctttctcctgtttctgcaagtgtcctgaaa 1557
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    327 AAGAAAAGAATAAAATACAGTGTTGGATCCCTTTCTCCTGTTTCTGCAAGTGTCCTGAAA 386

Qy   1558 aagactgaacaaaaggaaaaagtggaattgcaacatatttctcagaaagattgccaggaa 1617
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Db    387 AAGACTGAACAAAAGGAAAAAGTGGAATTGCAACATATTTCTCAGAAAGATTGCCAGGAA 446

Qy   1618 gatgatacaacagtgaaggagcagaatttcctgtataaagagacccaggaaactgaaaaa 1677
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    447 GATGATACAACAGTGAAGGAGCAGAATTTCCTGTATAAAGAGACCCAGGAAACTGAAAAA 506

Qy   1678 aagctcctgtttatttcagagcccatcccccacccttcaaatgaattgagagggcttaat 1737
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    507 AAGCTCCTGTTTATTTCAGAGCCCATCCCCCACCCTTCAAATGAATTGAGAGGGCTTAAT 566

Qy   1738 gagaaaatgagtaataaatgttccatgttaagtacagctgaagatgacataagacagaat 1797
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    567 GAGAAAATGAGTAATAAATGTTCCATGTTAAGTACAGCTGAAGATGACATAAGACAGAAT 626
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Qy   1798 tttacacagctacctctacataaaaacaaacaggaatgcattcttgacatttccgaacac 1857
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    627 TTTACACAGCTACCTCTACATAAAAACAAACAGGAATGCATTCTTGACATTTCCGAACAC 686

Qy   1858 acattaagtgaaaatgacttagaaga 1883
          |||||||||||||||||||||||||
Db    687 ACATTAAGTGAAAATGACTTAGAAGA 712


RESULT  14
AW960753
LOCUS       AW960753      701 bp    mRNA            EST       01-JUN-2000
DEFINITION  EST372824 MAGE resequences, MAGF Homo sapiens cDNA, mRNA sequence.
ACCESSION   AW960753
VERSION     AW960753.1  GI:8150437
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 701)
  AUTHORS   Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C., Holt
            ,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
            Quackenbush,J.
  TITLE     Assessment of gene expression patterns in a model of colon tumor
            metastasis using a 19,200 element cDNA microarray
  JOURNAL   Unpublished (2000)
COMMENT     Contact: John Quackenbush
            The Institute for Genomic Research
            9712 Medical Center Dr., Rockville, MD 20850, USA
            Tel: 301 838 3528
            Fax: 301 838 0208
            Email: johnq@tigr.org
            Plate: 150
            Seq primer: Reverse.
FEATURES             Location/Qualifiers
     source          1. .701
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                     /db_xref="taxon:9606"
                     /clone_lib="MAGE resequences, MAGF"
                     /note="Vector: pBluescriptSKm"
BASE COUNT      240 a    140 c    147 g    173 t      1 others
ORIGIN


  Query Match             24.7%;  Score 671.4;  DB 10;  Length 701;
  Best Local Similarity   98.8%;  Pred. No. 4.1e-99;
  Matches  686;  Conservative    0;  Mismatches    7;  Indels    1;  Gaps    1;

Qy    429 ctgtcaacaggccgggggaagccgtgctttcgcggctgcccggtgcgacactttctccgg 488
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Db      1 CTGTCAACAGGCCGGGGGAAGCCGTGCTTTCGCGGCTGCCCGGTGCGACACTTTCTCCGG 60

Qy    489 acccagcatgtaggtgccgggcgactgccatgaactccggagccatgaggatccacagta 548
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     61 ACCCAGCATGTAGGTGCCGGGCGACTGCCATGAACTCCGGAGCCATGAGGATCCACAGTA 120

Qy    549 aaggacatttccagggtggaatccaagtcaaaaatgaaaaaaacagaccatctctgaaat 608
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    121 AAGGACATTTCCAGGGTGGAATCCAAGTCAAAAATGAAAAAAACAGACCATCTCTGAAAT 180

Qy    609 ctctgaaaactgataacaggccagaaaaatccaaatgtaagccactttggggaaaagtat 668
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    181 CTCTGAAAACTGATAACAGGCCAGAAAAATCCAAATGTAAGCCACTTTGGGGAAAAGTAT 240

Qy    669 tttaccttgacttaccttctgtcaccatatctgaaaaacttcaaaaggacattaaggatc 728
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    241 TTTACCTTGACTTACCTTCTGTCACCATATCTGAAAAACTTCAAAAGGACATTAAGGATC 300

Qy    729 tgggagggcgagttgaagaatttctcagcaaagatatcagttatcttatttcaaataaga 788
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Db    301 TGGGAGGGCGAGTTGAAGAATTTCTCAGCAAAGATATCAGTTATCTTATTTCAAATAAGA 360

Qy    789 aggaagctaaatttgcacaaaccttgggtcgaatttctcctgtaccaagtccagaatctg 848
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Db    361 AGGAAGCTAAATTTGCACAAACCTTGGGTCGAATTTCTCCTGTACCAAGTCCAGAATCTG 420

Qy    849 catatactgcagaaaccacttcacctcatcccagccatgatggaagttcatttaagtcac 908
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    421 CATATACTGCAGAAACCACTTCACCTCATCCCAGCCATGATGGAAGTTCATTTAAGTCAC 480

Qy    909 cagacacagtgtgtttaagcagaggaaaattattagttgaaaaagctatcaaggaccatg 968
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Db    481 CAGACACAGTGTGTTTAAGCAGAGGAAAATTATTAGTTGAAAAAGCTATCAAGGACCATG 540

Qy    969 attttattccttcaaatagtatattatcaaatgccttgtcat-ggggagtaaaaattctt 1027
          ||| |||||||||||||||||||||||||||||||||||||| |||||||||||||||||
Db    541 ATTNTATTCCTTCAAATAGTATATTATCAAATGCCTTGTCATGGGGGAGTAAAAATTCTT 600

Qy   1028 catattgatgacattagatactacattgaacaaaagaaaaaagagttgtatttactcaag 1087
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Db    601 CATATGGATGACATTAGATACTACATTGAACAAAAGAAAAAAGAAGTGTATTTACTCAAG 660

Qy   1088 aaatcaagtacttcagtaagagatgggggcaaaa 1121
          |||||||||||||| | |||||||||||||| |||
Db    661 AAATCAAGTACTTTAATAAGAGATGGGGGCCAAA 694


RESULT  15
AI761101/c
LOCUS       AI761101      743 bp    mRNA            EST       21-DEC-1999
DEFINITION  wi69g03.x1 NCI_CGAP_Kid12 Homo sapiens cDNA clone IMAGE:2398612 3'
            similar to TR:O75226 O75226 WUGSC:H_RG135C18.1 PROTEIN ;, mRNA
            sequence.
ACCESSION   AI761101
VERSION     AI761101.1  GI:5176768
KEYWORDS    EST.
SOURCE      human.
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 743)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R.
            Emmert-Buck, M.D., Ph.D.
             cDNA Library Preparation: M. Bento Soares, Ph.D.
             cDNA Library Arrayed by: Greg Lennon, Ph.D.
             DNA Sequencing by: Washington University Genome Sequencing Center
             Clone distribution: NCI-CGAP clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            www-bio.llnl.gov/bbrp/image/image.html
            Insert Length: 1678   Std Error: 0.00
            Seq primer: -40UP from Gibco
            High quality sequence stop: 437.
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9606"
                     /clone="IMAGE:2398612"
                     /clone_lib="NCI_CGAP_Kid12"
                     /tissue_type="2 pooled tumors (clear cell type)"
                     /lab_host="DH10B"
                     /note="Organ: kidney; Vector: pT7T3D-Pac (Pharmacia) with
                     a modified polylinker; Site_1: Not I; Site_2: Eco RI;
                     Plasmid DNA from the normalized library NCI_CGAP_Kid5 was
                     prepared, and ss circles were made in vitro. Following HAP
                     purification, this DNA was used as tracer in a subtractive
                     hybridization reaction. The driver was PCR-amplified cDNAs
                     from a pool of 5,000 clones made from the same library
                     (cloneIDs 1323912-1325831, 1471368-1472903 and
                     1492104-1493255). Subtraction by Bento Soares and M.
```

Fatima Bonaldo. "
BASE COUNT 227 a 124 c 115 g 277 t
ORIGIN

Query Match 24.3%; Score 661.4; DB 10; Length 743;
Best Local Similarity 97.2%; Pred. No. 1.7e-97;
Matches 716; Conservative 0; Mismatches 16; Indels 5; Gaps 4;

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Qy   1933 tctgatttcagtacagataatagtggatctcaaccaaaacagaagtcagatactgtgctt 1992
          |||||||||||||||||| |||||||      | | | ||||||||||||||||||||| |
Db    743 TCTGATTTCAGTACAGATGATAGTGG--TCTCATCGAGACAGAAGTCAGATACTGTGC-T 687

Qy   1993 tttccagcaaaggatctcaaggaaaaggaccttcattcaatatttactcatgattctggt 2052
          ||||||||||||||||||||||||| |||||||||||||||||||||||||||||||||
Db    686 TTTCCAGCAAAGGATCTCAAGGAAACGGACCTTCATTCAATATTTACTCATGATTCTGGT 627

Qy   2053 ctgataacaataaacagttcacaagagcacctaactgttcaggcaaaggctccattccat 2112
          ||||||| |||||| |||||||||||||||||||||| |||| ||||||||||||||||    .
Db    626 CTGATATCAATAAGCAGTTCACAAGAGCACCTAACTG-TCAGTCAAAGGCTCCATTCCAT 568

Qy   2113 actcctcctgaggaacccaatgaatgtgacttcaagaatatggatagtttaccttctggt 2172
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    567 ACTCCTCCTGAGGAACCCAATGAATGTGACTTCAAGAATATGGATAGTTTACCTTCTGGT 508

Qy   2173 aaaatacatcgaaaagtgaaaataatattaggacgaaatagaaaagaaaatctggaacca 2232
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    507 AAAATACATCGAAAAGTGAAAATAATATTAGGACGAAATAGAAAAGAAAATCTGGAACCG 448

Qy   2233 aatgctgaatttgataaaagaactgaatttattacacaagaagaaaacagaatttgtagt 2292
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    447 AATGCTGAATTTGATAAAAGAACTGAATTTATTACACAAGAAGAAAACAGAATTTGTAGT 388

Qy   2293 tcaccggtacagtctttactagacttgtttcagactagtgaagagaaatcagaatttttg 2352
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    387 TCACCGGTACAGTCTTTACTAGACTTGTTTCAGACTAGTGAAGAGAAATCAGAATTTTTG 328

Qy   2353 ggtttcacaagctacacagaaaagagtggtatatgcaatg-ttttagatatttgggaaga 2411
          |||||||||||||||||||||||||||||||||||||| |||||||||||||||||||||
Db    327 GGTTTCACAAGCTACACAGAAAAGAGTGGTATATGCAATGTTTTTAGATATTTGGGAAGA 268

Qy   2412 ggaaaattcagataatctgttaacagcgtttttctcgtcccccttcaacttctacatttac 2471
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    267 GGAAAATTCAGATAATCTGTTAACAGCGTTTTTCTCGTCCCCTTCAACTTCTACATTTAC 208

Qy   2472 tggcttttagaatttaaaaaatgcatacttttcagaagtgataaggatcatattcttgaa 2531
          ||||||||||||||||||.||||||||||||||||||||||||||||||||||||||||||
Db    207 TGGCTTTTAGAATTTAAAAAATGCATACTTTTCAGAAGTGATAAGGATCATATTCTTGAA 148

Qy   2532 atttttataaatatgtatggaaattcttaggatttttttaccagctttgtttacagaccc 2591
          ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    147 ATTTTTATAAATATGTATGGAAATTCTTAGGATTTTTTTACCAGCTTTGTTTACAGACCC 88

Qy   2592 aaatgtaaatattaaaaataaatatttgcaattttctacagaattgaatacctgttaaag 2651
          |||||||||||||||||||||||||||| ||||||||||||||||||||||||||||||
Db     87 AAATGTAAATATTAAAAATAAATATTTGCCATTTTCTACAGAATTGAATACCTGTTAAAA 28

Qy   2652 aaaaattacagaataaa 2668
          ||||||||||||| |||
Db     27 AAAAATTACAGAAAAAA 11
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Job time: 4699 sec